

SEQUENCE LISTING

<110> Hammer, Philip E.
Hinson, Todd K.
Carr, Brian
Duck, Nicholas B.

<120> GDC-1 GENES CONFERRING HERBICIDE
RESISTANCE

<130> 045600/275114

<150> 60/453,237
<151> 2003-03-10

<160> 21

<170> FastSEQ for Windows Version 4.0

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<212> DNA
<213> Unknown

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<221> CDS
<222> (224) . . . (1951)

<223> Fungal isolate from soil sample

<400> 1

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ctgccccctcc atctgatacc taccttacat tgtcgccaac acacctataa gccataatat 180
accgactcaa agcaaaccac gcccattgtt tgattgtta atc atg gcc agc atc 235
                                         Met Ala Ser Ile
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aac atc agg gtg cag aat ctc gag caa ccc atg gac gtt gcc gag tat      283
Asn Ile Arg Val Gln Asn Leu Glu Gln Pro Met Asp Val Ala Glu Tyr
      5           10          15          20

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ctt ttt cg²⁵ g cgt ctc cac gaa atc gg³⁰ c att cgc tcc atc cac ggt ctt 331
 Leu Phe Arg Arg Leu His Glu Ile Gly Ile Arg Ser Ile His Gly Leu
25 30 35

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cca ggc gat tac aac ctt ctt gcc ctc gac tat ttg cca tca tgt ggc      379
Pro Gly Asp Tyr Asn Leu Leu Ala Leu Asp Tyr Leu Pro Ser Cys Gly
        40          45          50

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ctg aga tgg gtt ggc agc gtc aac gaa ctc aat gct gct tat gct gct 427
Leu Arg Trp Val Gly Ser Val Asn Glu Leu Asn Ala Ala Tyr Ala Ala
55 60 65

gat ggc tat gcc cgc gtc aag cag atg gga gct ctc atc acc act ttt			475
Asp Gly Tyr Ala Arg Val Lys Gln Met Gly Ala Leu Ile Thr Thr Phe			
70	75	80	
gga gtg gga gag ctc tca gcc atc aat ggc gtt gcc ggt gcc ttt tcg			523
Gly Val Gly Glu Leu Ser Ala Ile Asn Gly Val Ala Gly Ala Phe Ser			
85	90	95	100
gaa cac gtc cca gtc gtt cac att gtt ggc tgc cct tcc act gtc tcg			571
Glu His Val Pro Val Val His Ile Val Gly Cys Pro Ser Thr Val Ser			
105	110	115	
cag cga aac ggc atg ctc ctc cac cac acg ctt gga aac ggc gac ttc			619
Gln Arg Asn Gly Met Leu Leu His His Thr Leu Gly Asn Gly Asp Phe			
120	125	130	
aac atc ttt gcc aac atg agc gct caa atc tct tgc gaa gtg gcc aag			667
Asn Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys Glu Val Ala Lys			
135	140	145	
ctc acc aac cct gcc gaa att gcg acc cag atc gac cat gcc ctc cgc			715
Leu Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp His Ala Leu Arg			
150	155	160	
gtt tgc ttc att cgt tct cgg ccc gtc tac atc atg ctt ccc acc gat			763
Val Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met Leu Pro Thr Asp			
165	170	175	180
atg gtc cag gcc aaa gta gaa ggt gcc aga ctc aag gaa cca att gac			811
Met Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys Glu Pro Ile Asp			
185	190	195	
ttg tcg gag cct cca aat gat ccc gag aaa gaa gca tac gtc gtt gac			859
Leu Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala Tyr Val Val Asp			
200	205	210	
gtt gtc ctc aag tay ctc cgt gct gca aag aac ccc gtc atc ctt gtc			907
Val Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro Val Ile Leu Val			
215	220	225	
gat gct tgt gct atc cgt cat cgt gtt ctt gat gag gtt cat gat ctc			955
Asp Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu Val His Asp Leu			
230	235	240	
atc gaa aag aca aac ctc cct gtc ttt gtc act cct atg ggc aaa ggt			1003
Ile Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro Met Gly Lys Gly			
245	250	255	260
gct gtt aac gaa gaa cac ccg aca tat ggt ggt gtc tat gcc ggt gac			1051
Ala Val Asn Glu Glu His Pro Thr Tyr Gly Gly Val Tyr Ala Gly Asp			
265	270	275	
ggc tca cat ccg cct caa gtt aag gac atg gtt gag tct tct gat ttg			1099
Gly Ser His Pro Pro Gln Val Lys Asp Met Val Glu Ser Ser Asp Leu			
280	285	290	

ata ttg aca atc ggt gct ctc aag agc gac ttc aac act gct ggc ttc Ile Leu Thr Ile Gly Ala Leu Lys Ser Asp Phe Asn Thr Ala Gly Phe	295	300	305	1147
tct tac cgt acc tca cag ctg aac acg att gat cta cac agc gac cac Ser Tyr Arg Thr Ser Gln Leu Asn Thr Ile Asp Leu His Ser Asp His	310	315	320	1195
tgc att gtc aaa tac tcg aca tat cca ggt gtc cag atg agg ggt gtg Cys Ile Val Lys Tyr Ser Thr Tyr Pro Gly Val Gln Met Arg Gly Val	325	330	335	1243
ctg cga caa gtg att aag cag ctc gat gca tct gag atc aac gct cag Leu Arg Gln Val Ile Lys Gln Leu Asp Ala Ser Glu Ile Asn Ala Gln	345	350	355	1291
cca gcg cca gtc gtc gag aat gaa gtt gcc aaa aac cga gat aac tca Pro Ala Pro Val Val Glu Asn Glu Val Ala Lys Asn Arg Asp Asn Ser	360	365	370	1339
ccc gtc att aca caa gct ttc ttc tgg ccg cgc gtg gga gag ttc ctg Pro Val Ile Thr Gln Ala Phe Phe Trp Pro Arg Val Gly Glu Phe Leu	375	380	385	1387
aag aag aac gac atc gtc att acc gag act gga aca gcc aac ttt ggc Lys Lys Asn Asp Ile Val Ile Thr Glu Thr Gly Thr Ala Asn Phe Gly	390	395	400	1435
atc tgg gat act aag ttt ccc tct ggc gtt act gcg ctt tct cag gtc Ile Trp Asp Thr Lys Phe Pro Ser Gly Val Thr Ala Leu Ser Gln Val	405	410	415	420
ctt tgg gga agc att ggt tgg tcc gtt ggt gcc tgc caa gga gcc gtt Leu Trp Gly Ser Ile Gly Trp Ser Val Gly Ala Cys Gln Gly Ala Val	425	430	435	1531
ctt gca gcc gcc gat gac aac agc gat cgc aga act atc ctc ttt gtt Leu Ala Ala Ala Asp Asp Asn Ser Asp Arg Arg Thr Ile Leu Phe Val	440	445	450	1579
ggg gat ggc tca ttc cag ctc act gct caa gaa ttg agc aca atg att Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Leu Ser Thr Met Ile	455	460	465	1627
cgt ctc aag ctg aag ccc atc atc ttt gtc atc tgc aac gat ggc ttt Arg Leu Lys Leu Lys Pro Ile Ile Phe Val Ile Cys Asn Asp Gly Phe	470	475	480	1675
acc att gaa cga ttc att cac ggc atg gaa gcc gag tac aac gac atc Thr Ile Glu Arg Phe Ile His Gly Met Glu Ala Glu Tyr Asn Asp Ile	485	490	495	500
gca aat tgg gac ttc aag gct ctg gtt gac gtc ttt ggc ggc tct aag Ala Asn Trp Asp Phe Lys Ala Leu Val Asp Val Phe Gly Gly Ser Lys	505	510	515	1771
acg gcc aag aag ttc gcc gtc aag acc aac gac gag ctg gac agc ctt				1819

Thr Ala Lys Lys Phe Ala Val Lys Thr Lys Asp Glu Leu Asp Ser Leu			
520	525	530	
ctc aca gac cct acc ttt aac gcc gca gaa tgc ctc cag ttt gtc gag			1867
Leu Thr Asp Pro Thr Phe Asn Ala Ala Glu Cys Leu Gln Phe Val Glu			
535	540	545	
cta tat atg ccc aaa gaa gat gct cct cga gca ttg atc atg act gca			1915
Leu Tyr Met Pro Lys Glu Asp Ala Pro Arg Ala Leu Ile Met Thr Ala			
550	555	560	
gaa gct agc gcg agg aac aat gcc aag aca gag taa agtggactgt			1961
Glu Ala Ser Ala Arg Asn Asn Ala Lys Thr Glu *			
565	570	575	
catgaaggcc gatttaccac ctcataaatt gtaatagacc tgatacacat agatcaaggc	2021		
aggtaaccat cattaatcaa gcaggttgg atggggagg atttgaaaa tgagggaaacg	2081		
atgggatgtat atttggata actggccatt attttgatcttataaaaca aatttgaagt	2141		
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aaaaaaaaaaa	2210		
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<223> Fungal isolate from soil sample			
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Met Ala Ser Ile Asn Ile Arg Val Gln Asn Leu Glu Gln Pro Met Asp			
1	5	10	15
gtt gcc gag tat ctt ttt cggt ctc cac gaa atc ggc att cgc tcc	96		
Val Ala Glu Tyr Leu Phe Arg Arg Leu His Glu Ile Gly Ile Arg Ser			
20	25	30	
atc cac ggt ctt cca ggc gat tac aac ctt ctt gcc ctc gac tat ttg	144		
Ile His Gly Leu Pro Gly Asp Tyr Asn Leu Leu Ala Leu Asp Tyr Leu			
35	40	45	
cca tca tgt ggc ctg aga tgg gtt ggc agc gtc aac gaa ctc aat gct	192		
Pro Ser Cys Gly Leu Arg Trp Val Gly Ser Val Asn Glu Leu Asn Ala			
50	55	60	
gct tat gct gct gat ggc tat gcc cgc gtc aag cag atg gga gct ctc	240		
Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Val Lys Gln Met Gly Ala Leu			
65	70	75	80
atc acc act ttt gga gtg gga gag ctc tca gcc atc aat ggc gtt gcc	288		
Ile Thr Thr Phe Gly Val Gly Glu Leu Ser Ala Ile Asn Gly Val Ala			
85	90	95	

ggt gcc ttt tcg gaa cac gtc cca gtc gtt cac att gtt ggc tgc cct		336	
Gly Ala Phe Ser Glu His Val Pro Val Val His Ile Val Gly Cys Pro			
100	105	110	
tcc act gtc tcg cag cga aac ggc atg ctc ctc cac cac acg ctt gga		384	
Ser Thr Val Ser Gln Arg Asn Gly Met Leu Leu His His Thr Leu Gly			
115	120	125	
aac ggc gac ttc aac atc ttt gcc aac atg agc gct caa atc tct tgc		432	
Asn Gly Asp Phe Asn Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys			
130	135	140	
gaa gtg gcc aag ctc acc aac cct gcc gaa att gcg acc cag atc gac		480	
Glu Val Ala Lys Leu Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp			
145	150	155	160
cat gcc ctc cgc gtt tgc ttc att cgt tct cgg ccc gtc tac atc atg		528	
His Ala Leu Arg Val Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met			
165	170	175	
ctt ccc acc gat atg gtc cag gcc aaa gta gaa ggt gcc aga ctc aag		576	
Leu Pro Thr Asp Met Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys			
180	185	190	
gaa cca att gac ttg tcg gag cct cca aat gat ccc gag aaa gaa gca		624	
Glu Pro Ile Asp Leu Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala			
195	200	205	
tac gtc gtt gac gtt gtc ctc aag tay ctc cgt gct gca aag aac ccc		672	
Tyr Val Val Asp Val Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro			
210	215	220	
gtc atc ctt gtc gat gct tgt gct atc cgt cat cgt gtt ctt gat gag		720	
Val Ile Leu Val Asp Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu			
225	230	235	240
gtt cat gat ctc atc gaa aag aca aac ctc cct gtc ttt gtc act cct		768	
Val His Asp Leu Ile Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro			
245	250	255	
atg ggc aaa ggt gct gtt aac gaa gaa cac ccg aca tat ggt ggt gtc		816	
Met Gly Lys Gly Ala Val Asn Glu Glu His Pro Thr Tyr Gly Val			
260	265	270	
tat gcc ggt gac ggc tca cat ccg cct caa gtt aag gac atg gtt gag		864	
Tyr Ala Gly Asp Gly Ser His Pro Pro Gln Val Lys Asp Met Val Glu			
275	280	285	
tct tct gat ttg ata ttg aca atc ggt gct ctc aag agc gac ttc aac		912	
Ser Ser Asp Leu Ile Leu Thr Ile Gly Ala Leu Lys Ser Asp Phe Asn			
290	295	300	
act gct ggc ttc tct tac cgt acc tca cag ctg aac acg att gat cta		960	
Thr Ala Gly Phe Ser Tyr Arg Thr Ser Gln Leu Asn Thr Ile Asp Leu			
305	310	315	320
cac agc gac cac tgc att gtc aaa tac tcg aca tat cca ggt gtc cag		1008	

His Ser Asp His Cys Ile Val Lys Tyr Ser Thr Tyr Pro Gly Val Gln			
325	330	335	
atg agg ggt gtg ctg cga caa gtg att aag cag ctc gat gca tct gag			1056
Met Arg Gly Val Leu Arg Gln Val Ile Lys Gln Leu Asp Ala Ser Glu			
340	345	350	
atc aac gct cag cca gcg cca gtc gtc gag aat gaa gtt gcc aaa aac			1104
Ile Asn Ala Gln Pro Ala Pro Val Val Glu Asn Glu Val Ala Lys Asn			
355	360	365	
cga gat aac tca ccc gtc att aca caa gct ttc ttc tgg ccg cgc gtg			1152
Arg Asp Asn Ser Pro Val Ile Thr Gln Ala Phe Phe Trp Pro Arg Val			
370	375	380	
gga gag ttc ctg aag aac gac atc gtc att acc gag act gga aca			1200
Gly Glu Phe Leu Lys Lys Asn Asp Ile Val Ile Thr Glu Thr Gly Thr			
385	390	395	400
gcc aac ttt ggc atc tgg gat act aag ttt ccc tct ggc gtt act gcg			1248
Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe Pro Ser Gly Val Thr Ala			
405	410	415	
ctt tct cag gtc ctt tgg gga agc att ggt tgg tcc gtt ggt gcc tgc			1296
Leu Ser Gln Val Leu Trp Gly Ser Ile Gly Trp Ser Val Gly Ala Cys			
420	425	430	
caa gga gcc gtt ctt gca gcc gcc gat gac aac agc gat cgc aga act			1344
Gln Gly Ala Val Leu Ala Ala Ala Asp Asp Asn Ser Asp Arg Arg Thr			
435	440	445	
atc ctc ttt gtt ggt gat ggc tca ttc cag ctc act gct caa gaa ttg			1392
Ile Leu Phe Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Leu			
450	455	460	
agc aca atg att cgt ctc aag ctg aag ccc atc atc ttt gtc atc tgc			1440
Ser Thr Met Ile Arg Leu Lys Leu Lys Pro Ile Ile Phe Val Ile Cys			
465	470	475	480
aac gat ggc ttt acc att gaa cga ttc att cac ggc atg gaa gcc gag			1488
Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile His Gly Met Glu Ala Glu			
485	490	495	
tac aac gac atc gca aat tgg gac ttc aag gct ctg gtt gac gtc ttt			1536
Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys Ala Leu Val Asp Val Phe			
500	505	510	
ggc ggc tct aag acg gcc aag aag ttc gcc gtc aag acc aag gac gag			1584
Gly Gly Ser Lys Thr Ala Lys Lys Phe Ala Val Lys Thr Lys Asp Glu			
515	520	525	
ctg gac agc ctt ctc aca gac cct acc ttt aac gcc gca gaa tgc ctc			1632
Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe Asn Ala Ala Glu Cys Leu			
530	535	540	
cag ttt gtc gag cta tat atg ccc aaa gaa gat gct cct cga gca ttg			1680
Gln Phe Val Glu Leu Tyr Met Pro Lys Glu Asp Ala Pro Arg Ala Leu			

atc atg act gca gaa gct agc gcg agg aac aat gcc aag aca gag 1725
 Ile Met Thr Ala Glu Ala Ser Ala Arg Asn Asn Ala Lys Thr Glu
 565 570 575

<210> 3
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<212> PRT
<213> Unknown

<220>
<223> Fungal isolate from soil sample

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 340 345 350
 Ile Asn Ala Gln Pro Ala Pro Val Val Glu Asn Glu Val Ala Lys Asn
 355 360 365
 Arg Asp Asn Ser Pro Val Ile Thr Gln Ala Phe Phe Trp Pro Arg Val
 370 375 380
 Gly Glu Phe Leu Lys Lys Asn Asp Ile Val Ile Thr Glu Thr Gly Thr
 385 390 395 400
 Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe Pro Ser Gly Val Thr Ala
 405 410 415
 Leu Ser Gln Val Leu Trp Gly Ser Ile Gly Trp Ser Val Gly Ala Cys
 420 425 430
 Gln Gly Ala Val Leu Ala Ala Asp Asp Asn Ser Asp Arg Arg Thr
 435 440 445
 Ile Leu Phe Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Leu
 450 455 460
 Ser Thr Met Ile Arg Leu Lys Leu Lys Pro Ile Ile Phe Val Ile Cys
 465 470 475 480
 Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile His Gly Met Glu Ala Glu
 485 490 495
 Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys Ala Leu Val Asp Val Phe
 500 505 510
 Gly Gly Ser Lys Thr Ala Lys Lys Phe Ala Val Lys Thr Lys Asp Glu
 515 520 525
 Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe Asn Ala Ala Glu Cys Leu
 530 535 540
 Gln Phe Val Glu Leu Tyr Met Pro Lys Glu Asp Ala Pro Arg Ala Leu
 545 550 555 560
 Ile Met Thr Ala Glu Ala Ser Ala Arg Asn Asn Ala Lys Thr Glu
 565 570 575

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<220>
 <221> CDS
 <222> (3)...(596)

<223> Fungal isolate from soil sample

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 Phe Phe Trp Pro Arg Val Gly Glu Phe Leu Lys Lys Asn Asp Ile
 1 5 10 15

 gtc att acc gag act gga aca gcc aac ttt ggc atc tgg gat act aag 95
 Val Ile Thr Glu Thr Gly Thr Ala Asn Phe Gly Ile Trp Asp Thr Lys
 20 25 30

 ttt ccc tct ggc gtt act gcg ctt tct cag gtc ctt tgg gga agc att 143
 Phe Pro Ser Gly Val Thr Ala Leu Ser Gln Val Leu Trp Gly Ser Ile
 35 40 45

ggt tgg tcc gtt ggt gcc tgc caa gga gcc gtt ctt gca gcc gcc gat		191
Gly Trp Ser Val Gly Ala Cys Gln Gly Ala Val Leu Ala Ala Ala Asp		
50	55	60
gac aac agc gat cgc aga act atc ctc ttt gtt ggt gat ggc tca ttc		239
Asp Asn Ser Asp Arg Arg Thr Ile Leu Phe Val Gly Asp Gly Ser Phe		
65	70	75
cag ctc act gct caa gaa ttg agc aca atg att cgt ctc aag ctg aag		287
Gln Leu Thr Ala Gln Glu Leu Ser Thr Met Ile Arg Leu Lys Leu Lys		
80	85	90
ccc atc atc ttt gtc atc tgc aac gat ggc ttt acc att gaa cga ttc		335
Pro Ile Ile Phe Val Ile Cys Asn Asp Gly Phe Thr Ile Glu Arg Phe		
100	105	110
att cac ggc atg gaa gcc gag tac aac gac atc gca aat tgg gac ttc		383
Ile His Gly Met Glu Ala Glu Tyr Asn Asp Ile Ala Asn Trp Asp Phe		
115	120	125
aag gct ctg gtt gac gtc ttt ggc ggc tct aag acg gcc aag aag ttc		431
Lys Ala Leu Val Asp Val Phe Gly Gly Ser Lys Thr Ala Lys Lys Phe		
130	135	140
gcc gtc aag acc aag gac gag ctg gac agc ctt ctc aca gac cct acc		479
Ala Val Lys Thr Lys Asp Glu Leu Asp Ser Leu Leu Thr Asp Pro Thr		
145	150	155
ttt aac gcc gca gaa tgc ctc cag ttt gtc gag cta tat atg ccc aaa		527
Phe Asn Ala Ala Glu Cys Leu Gln Phe Val Glu Leu Tyr Met Pro Lys		
160	165	170
gaa gat gct cct cga gca ttg atc atg act gca gaa gct agc gcg agg		575
Glu Asp Ala Pro Arg Ala Leu Ile Met Thr Ala Glu Ala Ser Ala Arg		
180	185	190
aac aat gcc aag aca gag taa agtggactgt catgaaggcc gatttaccac		626
Asn Asn Ala Lys Thr Glu *		
195		
ctcataaaatt gtaatagacc tgatacacat agatcaaggc aggtaccgat cattaatcaa	686	
gcaggtttgg atgggaaagg atttgaaaaa tgaggaaacg atggatgat atttggaata	746	
actggccatt atttgagta cttataaaca aatttgaagt tcaattttt ttcaaaaaaaaa	806	
aaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa	835	

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<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (1)...(591)

<223> Fungal isolate from soil sample

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 1 5 10 15

 att acc gag act gga aca gcc aac ttt ggc atc tgg gat act aag ttt 96
 Ile Thr Glu Thr Gly Thr Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe
 20 25 30

 ccc tct ggc gtt act gcg ctt tct cag gtc ctt tgg gga agc att ggt 144
 Pro Ser Gly Val Thr Ala Leu Ser Gln Val Leu Trp Gly Ser Ile Gly
 35 40 45

 tgg tcc gtt ggt gcc tgc caa gga gcc gtt ctt gca gcc gcc gat gac 192
 Trp Ser Val Gly Ala Cys Gln Gly Ala Val Leu Ala Ala Asp Asp
 50 55 60

 aac agc gat cgc aga act atc ctc ttt gtt ggt gat ggc tca ttc cag 240
 Asn Ser Asp Arg Arg Thr Ile Leu Phe Val Gly Asp Gly Ser Phe Gln
 65 70 75 80

 ctc act gct caa gaa ttg agc aca atg att cgt ctc aag ctg aag ccc 288
 Leu Thr Ala Gln Glu Leu Ser Thr Met Ile Arg Leu Lys Leu Lys Pro
 85 90 95

 atc atc ttt gtc atc tgc aac gat ggc ttt acc att gaa cga ttc att 336
 Ile Ile Phe Val Ile Cys Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile
 100 105 110

 cac ggc atg gaa gcc gag tac aac gac atc gca aat tgg gac ttc aag 384
 His Gly Met Glu Ala Glu Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys
 115 120 125

 gct ctg gtt gac gtc ttt ggc ggc tct aag acg gcc aag aag ttc gcc 432
 Ala Leu Val Asp Val Phe Gly Ser Lys Thr Ala Lys Lys Phe Ala
 130 135 140

 gtc aag acc aag gac gag ctg gac agc ctt ctc aca gac cct acc ttt 480
 Val Lys Thr Lys Asp Glu Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe
 145 150 155 160

 aac gcc gca gaa tgc ctc cag ttt gtc gag cta tat atg ccc aaa gaa 528
 Asn Ala Ala Glu Cys Leu Gln Phe Val Glu Leu Tyr Met Pro Lys Glu
 165 170 175

 gat gct cct cga gca ttg atc atg act gca gaa gct agc gcg agg aac 576
 Asp Ala Pro Arg Ala Leu Ile Met Thr Ala Glu Ala Ser Ala Arg Asn
 180 185 190

 aat gcc aag aca gag 591
 Asn Ala Lys Thr Glu
 195

<210> 6
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<213> Unknown

<220>

<223> Fungal isolate from soil sample

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1 5 10 15
Ile Thr Glu Thr Gly Thr Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe
20 25 30
Pro Ser Gly Val Thr Ala Leu Ser Gln Val Leu Trp Gly Ser Ile Gly
35 40 45
Trp Ser Val Gly Ala Cys Gln Gly Ala Val Leu Ala Ala Ala Asp Asp
50 55 60
Asn Ser Asp Arg Arg Thr Ile Leu Phe Val Gly Asp Gly Ser Phe Gln
65 70 75 80
Leu Thr Ala Gln Glu Leu Ser Thr Met Ile Arg Leu Lys Leu Lys Pro
85 90 95
Ile Ile Phe Val Ile Cys Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile
100 105 110
His Gly Met Glu Ala Glu Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys
115 120 125
Ala Leu Val Asp Val Phe Gly Ser Lys Thr Ala Lys Lys Phe Ala
130 135 140
Val Lys Thr Lys Asp Glu Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe
145 150 155 160
Asn Ala Ala Glu Cys Leu Gln Phe Val Glu Leu Tyr Met Pro Lys Glu
165 170 175
Asp Ala Pro Arg Ala Leu Ile Met Thr Ala Glu Ala Ser Ala Arg Asn
180 185 190
Asn Ala Lys Thr Glu
195

<210> 7

<211> 678

<212> DNA

<213> Unknown

<220>

<221> CDS

<222> (1)...(678)

<223> Fungal isolate from soil sample

<400> 7

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Thr Tyr Pro Gly Val Gln Met Arg Gly Val Leu Arg Gln Val Ile Lys
1 5 10 15
cag ctc gat gca tct gag atc aac gct cag cca gcg cca gtc gtc gag 96
Gln Leu Asp Ala Ser Glu Ile Asn Ala Gln Pro Ala Pro Val Val Glu
20 25 30
aat gaa gtt gcc aaa aac cga gat aac tca ccc gtc att aca caa gct 144
Asn Glu Val Ala Lys Asn Arg Asp Asn Ser Pro Val Ile Thr Gln Ala
35 40 45

ttc ttc tgg ccg cgc gtg gga gag ttc ctg aag aag aac gac atc gtc		192	
Phe Phe Trp Pro Arg Val Gly Glu Phe Leu Lys Lys Asn Asp Ile Val			
50	55	60	
att acc gag act gga aca gcc aac ttt ggc atc tgg gat act aag ttt		240	
Ile Thr Glu Thr Gly Thr Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe			
65	70	75	80
ccc tct ggc gtt act gcg ctt tct cag gtc ctt tgg gga agc att ggt		288	
Pro Ser Gly Val Thr Ala Leu Ser Gln Val Leu Trp Gly Ser Ile Gly			
85	90	95	
tgg tcc gtt ggt gcc tgc caa gga gcc gtt ctt gca gcc gcc gat gac		336	
Trp Ser Val Gly Ala Cys Gln Gly Ala Val Leu Ala Ala Ala Asp Asp			
100	105	110	
aac agc gat cgc aga act atc ctc ttt gtt ggt gat ggc tca ttc cag		384	
Asn Ser Asp Arg Arg Thr Ile Leu Phe Val Gly Asp Gly Ser Phe Gln			
115	120	125	
ctc act gct caa gaa ttg agc aca atg att cgt ctc aag ctg aag ccc		432	
Leu Thr Ala Gln Glu Leu Ser Thr Met Ile Arg Leu Lys Leu Lys Pro			
130	135	140	
atc atc ttt gtc atc tgc aac gat ggc ttt acc att gaa cga ttc att		480	
Ile Ile Phe Val Ile Cys Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile			
145	150	155	160
cac ggc atg gaa gcc gag tac aac gac atc gca aat tgg gac ttc aag		528	
His Gly Met Glu Ala Glu Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys			
165	170	175	
gct ctg gtt gac gtc ttt ggc ggc tct aag acg gcc aag aag ttc gcc		576	
Ala Leu Val Asp Val Phe Gly Gly Ser Lys Thr Ala Lys Lys Phe Ala			
180	185	190	
gtc aag acc aag gac gag ctg gac agc ctt ctc aca gac cct acc ttt		624	
Val Lys Thr Lys Asp Glu Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe			
195	200	205	
aac gcc gca gaa tgc ctc cag ttt gtc gag cta tat atg ccc aaa gaa		672	
Asn Ala Ala Glu Cys Leu Gln Phe Val Glu Leu Tyr Met Pro Lys Glu			
210	215	220	
gat gct		678	
Asp Ala			
225			

<210> 8
<211> 226
<212> PRT
<213> Unknown

<220>
<223> Fungal isolate from soil sample

<400> 8

Thr	Tyr	Pro	Gly	Val	Gln	Met	Arg	Gly	Val	Leu	Arg	Gln	Val	Ile	Lys
1						5				10					15
Gln	Leu	Asp	Ala	Ser	Glu	Ile	Asn	Ala	Gln	Pro	Ala	Pro	Val	Val	Glu
						20				25					30
Asn	Glu	Val	Ala	Lys	Asn	Arg	Asp	Asn	Ser	Pro	Val	Ile	Thr	Gln	Ala
						35				40					45
Phe	Phe	Trp	Pro	Arg	Val	Gly	Glu	Phe	Leu	Lys	Lys	Asn	Asp	Ile	Val
						50				55					60
Ile	Thr	Glu	Thr	Gly	Thr	Ala	Asn	Phe	Gly	Ile	Trp	Asp	Thr	Lys	Phe
65						70				75					80
Pro	Ser	Gly	Val	Thr	Ala	Leu	Ser	Gln	Val	Leu	Trp	Gly	Ser	Ile	Gly
						85				90					95
Trp	Ser	Val	Gly	Ala	Cys	Gln	Gly	Ala	Val	Leu	Ala	Ala	Asp	Asp	
						100				105					110
Asn	Ser	Asp	Arg	Arg	Thr	Ile	Leu	Phe	Val	Gly	Asp	Gly	Ser	Phe	Gln
						115				120					125
Leu	Thr	Ala	Gln	Glu	Leu	Ser	Thr	Met	Ile	Arg	Leu	Lys	Leu	Lys	Pro
						130				135					140
Ile	Ile	Phe	Val	Ile	Cys	Asn	Asp	Gly	Phe	Thr	Ile	Glu	Arg	Phe	Ile
145						150				155					160
His	Gly	Met	Glu	Ala	Glu	Tyr	Asn	Asp	Ile	Ala	Asn	Trp	Asp	Phe	Lys
						165				170					175
Ala	Leu	Val	Asp	Val	Phe	Gly	Gly	Ser	Lys	Thr	Ala	Lys	Lys	Phe	Ala
						180				185					190
Val	Lys	Thr	Lys	Asp	Glu	Leu	Asp	Ser	Leu	Leu	Thr	Asp	Pro	Thr	Phe
						195				200					205
Asn	Ala	Ala	Glu	Cys	Leu	Gln	Phe	Val	Glu	Leu	Tyr	Met	Pro	Lys	Glu
						210				215					220
Asp	Ala														
		225													

<210> 9

<211> 1636

<212> DNA

<213> Unknown

<220>

<221> CDS

<222> (1) ... (1377)

<223> Fungal isolate from soil sample

<400> 9

cga	aac	ggc	atg	ctc	ctc	cac	cac	acg	ctt	gga	aac	ggc	gac	ttc	aac
Arg	Asn	Gly	Met	Leu	Leu	His	His	Thr	Leu	Gly	Asn	Gly	Asp	Phe	Asn
1			5						10						15

48

atc	ttt	gcc	aac	atg	agc	gct	caa	atc	tct	tgc	gaa	gtg	gcc	aag	ctc
Ile	Phe	Ala	Asn	Met	Ser	Ala	Gln	Ile	Ser	Cys	Glu	Val	Ala	Lys	Leu
															30

96

acc	aac	cct	gcc	gaa	att	gcg	acc	cag	atc	gac	cat	gcc	ctc	cgc	gtt
Thr	Asn	Pro	Ala	Glu	Ile	Ala	Thr	Gln	Ile	Asp	His	Ala	Leu	Arg	Val
															45
						35				40					

144

tgc ttc att cgt tct cgg ccc gtc tac atc atg ctt ccc acc gat atg Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met Leu Pro Thr Asp Met	50	55	60	192	
gtc cag gcc aaa gta gaa ggt gcc aga ctc aag gaa cca att gac ttg Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys Glu Pro Ile Asp Leu	65	70	75	80	240
tcg gag cct cca aat gat ccc gag aaa gaa gca tac gtc gtt gac gtt Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala Tyr Val Val Asp Val	85	90	95		288
gtc ctc aag tac ctc cgt gct gca aag aac ccc gtc atc ctt gtc gat Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro Val Ile Leu Val Asp	100	105	110		336
gct tgt gct atc cgt cat cgt gtt ctt gat gag gtt cat gat ctc atc Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu Val His Asp Leu Ile	115	120	125		384
gaa aag aca aac ctc cct gtc ttt gtc act cct atg ggc aaa ggt gct Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro Met Gly Lys Gly Ala	130	135	140		432
gtt aac gaa gaa cac ccg aca tat ggt ggt gtc tat gcc ggt gac ggc Val Asn Glu Glu His Pro Thr Tyr Gly Gly Val Tyr Ala Gly Asp Gly	145	150	155	160	480
tca cat ccg cct caa gtt aag gac atg gtt gag tct tct gat ttg ata Ser His Pro Pro Gln Val Lys Asp Met Val Glu Ser Ser Asp Leu Ile	165	170	175		528
ttg aca atc ggt gct ctc aag agc gac ttc aac act gct ggc ttc tct Leu Thr Ile Gly Ala Leu Lys Ser Asp Phe Asn Thr Ala Gly Phe Ser	180	185	190		576
tac cgt acc tca cag ctg aac acg att gat cta cac agc gac cac tgc Tyr Arg Thr Ser Gln Leu Asn Thr Ile Asp Leu His Ser Asp His Cys	195	200	205		624
att gtc aaa tac tcg aca tat cca ggt gtc cag atg agg ggt gtg ctg Ile Val Lys Tyr Ser Thr Tyr Pro Gly Val Gln Met Arg Gly Val Leu	210	215	220		672
cga caa gtg att aag cag ctc gat gca tct gag atc aac gct cag cca Arg Gln Val Ile Lys Gln Leu Asp Ala Ser Glu Ile Asn Ala Gln Pro	225	230	235	240	720
gcg cca gtc gag aat gaa gtt gcc aaa aac cga gat aac tca ccc Ala Pro Val Val Glu Asn Glu Val Ala Lys Asn Arg Asp Asn Ser Pro	245	250	255		768
gtc att aca caa gct ttc ttc tgg ccg cgc gtg gga gag ttc ctg aag Val Ile Thr Gln Ala Phe Phe Trp Pro Arg Val Gly Glu Phe Leu Lys	260	265	270		816

aag aac gac atc gtc att acc gag act gga aca gcc aac ttt ggc atc		864
Lys Asn Asp Ile Val Ile Thr Glu Thr Gly Thr Ala Asn Phe Gly Ile		
275	280	285
 tgg gat act aag ttt ccc tct ggc gtt act gcg ctt tct cag gtc ctt		912
Trp Asp Thr Lys Phe Pro Ser Gly Val Thr Ala Leu Ser Gln Val Leu		
290	295	300
 tgg gga agc att ggt tgg tcc gtt ggt gcc tgc caa gga gcc gtt ctt		960
Trp Gly Ser Ile Gly Trp Ser Val Gly Ala Cys Gln Gly Ala Val Leu		
305	310	315
 gca gcc gcc gat gac aac agc gat cgc aga act atc ctc ttt gtt ggt		1008
Ala Ala Ala Asp Asp Asn Ser Asp Arg Arg Thr Ile Leu Phe Val Gly		
325	330	335
 gat ggc tca ttc cag ctc act gct caa gaa ttg agc aca atg att cgt		1056
Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Leu Ser Thr Met Ile Arg		
340	345	350
 ctc aag ctg aag ccc atc atc ttt gtc atc tgc aac gat ggc ttt acc		1104
Leu Lys Leu Lys Pro Ile Ile Phe Val Ile Cys Asn Asp Gly Phe Thr		
355	360	365
 att gaa cga ttc att cac ggc atg gaa gcc gag tac aac gac atc gca		1152
Ile Glu Arg Phe Ile His Gly Met Glu Ala Glu Tyr Asn Asp Ile Ala		
370	375	380
 aat tgg gac ttc aag gct ctg gtt gac gtc ttt ggc ggc tct aag acg		1200
Asn Trp Asp Phe Lys Ala Leu Val Asp Val Phe Gly Gly Ser Lys Thr		
385	390	395
 gcc aag aag ttc gcc gtc aag acc aag gac gag ctg gac agc ctt ctc		1248
Ala Lys Lys Phe Ala Val Lys Thr Lys Asp Glu Leu Asp Ser Leu Leu		
405	410	415
 aca gac cct acc ttt aac gcc gca gaa tgc ctc cag ttt gtc gag cta		1296
Thr Asp Pro Thr Phe Asn Ala Ala Glu Cys Leu Gln Phe Val Glu Leu		
420	425	430
 tat atg ccc aaa gaa gat gct cct cga gca ttg atc atg act gca gaa		1344
Tyr Met Pro Lys Glu Asp Ala Pro Arg Ala Leu Ile Met Thr Ala Glu		
435	440	445
 gct agc gcg agg aac aat gcc aag aca gag taa agtggactgt catgaaggcc		1397
Ala Ser Ala Arg Asn Asn Ala Lys Thr Glu *		
450	455	
 gat tttaccac ctcataaaatt gtaatagacc tgatacacat agatcaaggc aggttaccat		1457
cattaatcaa gcagggttgg atggggaaagg attttgaaaa tgagggaaacg atgggatgtat		1517
atttggaata actggccatt attttgagta cttataaaca aatttgaagt tcaatttttt		1577
ttcaaa		1636

<210> 10
<211> 1374
<212> DNA
<213> Unknown

<220>
<221> CDS
<222> (1)...(1374)

<223> Fungal isolate from soil sample

<400> 10
cga aac ggc atg ctc ctc cac cac acg ctt gga aac ggc gac ttc aac 48
Arg Asn Gly Met Leu Leu His His Thr Leu Gly Asn Gly Asp Phe Asn
1 5 10 15

atc ttt gcc aac atg agc gct caa atc tct tgc gaa gtg gcc aag ctc 96
Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys Glu Val Ala Lys Leu
20 25 30

acc aac cct gcc gaa att gcg acc cag atc gac cat gcc ctc cgc gtt 144
Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp His Ala Leu Arg Val
35 40 45

tgc ttc att cgt tct cgg ccc gtc tac atc atg ctt ccc acc gat atg 192
Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met Leu Pro Thr Asp Met
50 55 60

gtc cag gcc aaa gta gaa ggt gcc aga ctc aag gaa cca att gac ttg 240
Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys Glu Pro Ile Asp Leu
65 70 75 80

tcg gag cct cca aat gat ccc gag aaa gaa gca tac gtc gtt gac gtt 288
Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala Tyr Val Val Asp Val
85 90 95

gtc ctc aag tac ctc cgt gct gca aag aac ccc gtc atc ctt gtc gat 336
Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro Val Ile Leu Val Asp
100 105 110

gct tgt gct atc cgt cat cgt gtt ctt gat gag gtt cat gat ctc atc 384
Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu Val His Asp Leu Ile
115 120 125

gaa aag aca aac ctc cct gtc ttt gtc act cct atg ggc aaa ggt gct 432
Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro Met Gly Lys Gly Ala
130 135 140

gtt aac gaa gaa cac ccg aca tat ggt ggt gtc tat gcc ggt gac ggc 480
Val Asn Glu Glu His Pro Thr Tyr Gly Gly Val Tyr Ala Gly Asp Gly
145 150 155 160

tca cat ccg cct caa gtt aag gac atg gtt gag tct tct gat ttg ata 528
Ser His Pro Pro Gln Val Lys Asp Met Val Glu Ser Ser Asp Leu Ile
165 170 175

ttg aca atc ggt gct ctc aag agc gac ttc aac act gct ggc ttc tct 576
Leu Thr Ile Gly Ala Leu Lys Ser Asp Phe Asn Thr Ala Gly Phe Ser
180 185 190

tac cgt acc tca cag ctg aac acg att gat cta cac agc gac cac tgc 624

Tyr Arg Thr Ser Gln Leu Asn Thr Ile Asp Leu His Ser Asp His Cys			
195	200	205	
att gtc aaa tac tcg aca tat cca ggt gtc cag atg agg ggt gtg ctg	672		
Ile Val Lys Tyr Ser Thr Tyr Pro Gly Val Gln Met Arg Gly Val Leu			
210	215	220	
cga caa gtg att aag cag ctc gat gca tct gag atc aac gct cag cca	720		
Arg Gln Val Ile Lys Gln Leu Asp Ala Ser Glu Ile Asn Ala Gln Pro			
225	230	235	240
gcg cca gtc gtc gag aat gaa gtt gcc aaa aac cga gat aac tca ccc	768		
Ala Pro Val Val Glu Asn Glu Val Ala Lys Asn Arg Asp Asn Ser Pro			
245	250	255	
gtc att aca caa gct ttc ttc tgg ccg cgc gtg gga gag ttc ctg aag	816		
Val Ile Thr Gln Ala Phe Phe Trp Pro Arg Val Gly Glu Phe Leu Lys			
260	265	270	
aag aac gac atc gtc att acc gag act gga aca gcc aac ttt ggc atc	864		
Lys Asn Asp Ile Val Ile Thr Glu Thr Gly Thr Ala Asn Phe Gly Ile			
275	280	285	
tgg gat act aag ttt ccc tct ggc gtt act gcg ctt tct cag gtc ctt	912		
Trp Asp Thr Lys Phe Pro Ser Gly Val Thr Ala Leu Ser Gln Val Leu			
290	295	300	
tgg gga agc att ggt tgg tcc gtt ggt gcc tgc caa gga gcc gtt ctt	960		
Trp Gly Ser Ile Gly Trp Ser Val Gly Ala Cys Gln Gly Ala Val Leu			
305	310	315	320
gca gcc gcc gat gac aac agc gat cgc aga act atc ctc ttt gtt ggt	1008		
Ala Ala Ala Asp Asp Asn Ser Asp Arg Arg Thr Ile Leu Phe Val Gly			
325	330	335	
gat ggc tca ttc cag ctc act gct caa gaa ttg agc aca atg att cgt	1056		
Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Leu Ser Thr Met Ile Arg			
340	345	350	
ctc aag ctg aag ccc atc atc ttt gtc atc tgc aac gat ggc ttt acc	1104		
Leu Lys Leu Lys Pro Ile Ile Phe Val Ile Cys Asn Asp Gly Phe Thr			
355	360	365	
att gaa cga ttc att cac ggc atg gaa gcc gag tac aac gac atc gca	1152		
Ile Glu Arg Phe Ile His Gly Met Glu Ala Glu Tyr Asn Asp Ile Ala			
370	375	380	
aat tgg gac ttc aag gct ctg gtt gac gtc ttt ggc ggc tct aag acg	1200		
Asn Trp Asp Phe Lys Ala Leu Val Asp Val Phe Gly Gly Ser Lys Thr			
385	390	395	400
gcc aag aag ttc gcc gtc aag acc aag gac gag ctg gac agc ctt ctc	1248		
Ala Lys Lys Phe Ala Val Lys Thr Lys Asp Glu Leu Asp Ser Leu Leu			
405	410	415	
aca gac cct acc ttt aac gcc gca gaa tgc ctc cag ttt gtc gag cta	1296		
Thr Asp Pro Thr Phe Asn Ala Ala Glu Cys Leu Gln Phe Val Glu Leu			

420

425

430

tat atg ccc aaa gaa gat gct cct cga gca ttg atc atg act gca gaa 1344
 Tyr Met Pro Lys Glu Asp Ala Pro Arg Ala Leu Ile Met Thr Ala Glu
 435 440 445

gct agc gcg agg aac aat gcc aag aca gag 1374
 Ala Ser Ala Arg Asn Asn Ala Lys Thr Glu
 450 455

<210> 11
 <211> 458
 <212> PRT
 <213> Unknown

<220>
 <223> Fungal isolate from soil sample

<400> 11
 Arg Asn Gly Met Leu Leu His His Thr Leu Gly Asn Gly Asp Phe Asn
 1 5 10 15
 Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys Glu Val Ala Lys Leu
 20 25 30
 Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp His Ala Leu Arg Val
 35 40 45
 Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met Leu Pro Thr Asp Met
 50 55 60
 Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys Glu Pro Ile Asp Leu
 65 70 75 80
 Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala Tyr Val Val Asp Val
 85 90 95
 Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro Val Ile Leu Val Asp
 100 105 110
 Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu Val His Asp Leu Ile
 115 120 125
 Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro Met Gly Lys Gly Ala
 130 135 140
 Val Asn Glu Glu His Pro Thr Tyr Gly Val Tyr Ala Gly Asp Gly
 145 150 155 160
 Ser His Pro Pro Gln Val Lys Asp Met Val Glu Ser Ser Asp Leu Ile
 165 170 175
 Leu Thr Ile Gly Ala Leu Lys Ser Asp Phe Asn Thr Ala Gly Phe Ser
 180 185 190
 Tyr Arg Thr Ser Gln Leu Asn Thr Ile Asp Leu His Ser Asp His Cys
 195 200 205
 Ile Val Lys Tyr Ser Thr Tyr Pro Gly Val Gln Met Arg Gly Val Leu
 210 215 220
 Arg Gln Val Ile Lys Gln Leu Asp Ala Ser Glu Ile Asn Ala Gln Pro
 225 230 235 240
 Ala Pro Val Val Glu Asn Glu Val Ala Lys Asn Arg Asp Asn Ser Pro
 245 250 255
 Val Ile Thr Gln Ala Phe Phe Trp Pro Arg Val Gly Glu Phe Leu Lys
 260 265 270
 Lys Asn Asp Ile Val Ile Thr Glu Thr Gly Thr Ala Asn Phe Gly Ile
 275 280 285
 Trp Asp Thr Lys Phe Pro Ser Gly Val Thr Ala Leu Ser Gln Val Leu

290	295	300
Trp Gly Ser Ile Gly Trp Ser Val Gly Ala Cys Gln Gly Ala Val Leu		
305	310	315
Ala Ala Ala Asp Asp Asn Ser Asp Arg Arg Thr Ile Leu Phe Val Gly		320
325	330	335
Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Leu Ser Thr Met Ile Arg		
340	345	350
Leu Lys Leu Lys Pro Ile Ile Phe Val Ile Cys Asn Asp Gly Phe Thr		
355	360	365
Ile Glu Arg Phe Ile His Gly Met Glu Ala Glu Tyr Asn Asp Ile Ala		
370	375	380
Asn Trp Asp Phe Lys Ala Leu Val Asp Val Phe Gly Gly Ser Lys Thr		
385	390	395
Ala Lys Lys Phe Ala Val Lys Thr Lys Asp Glu Leu Asp Ser Leu Leu		400
405	410	415
Thr Asp Pro Thr Phe Asn Ala Ala Glu Cys Leu Gln Phe Val Glu Leu		
420	425	430
Tyr Met Pro Lys Glu Asp Ala Pro Arg Ala Leu Ile Met Thr Ala Glu		
435	440	445
Ala Ser Ala Arg Asn Asn Ala Lys Thr Glu		
450	455	

<210> 12

<211> 30

<212> DNA

<213> Unknown

<220>

<221> CDS

<222> (1) . . . (30)

<223> Oligonucleotide used for PCR amplification of
GDC-1

<400> 12

tcc cag atg cca aag ttg gct gtt cca gtc		
Ser Gln Met Pro Lys Leu Ala Val Pro Val		
1	5	10

30

<210> 13

<211> 563

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 13

Met Ser Glu Ile Thr Leu Gly Lys Tyr Leu Phe Glu Arg Leu Lys Gln		
1	5	10
Val Asn Val Asn Thr Val Phe Gly Leu Pro Gly Asp Phe Asn Leu Ser		
20	25	30
Leu Leu Asp Lys Ile Tyr Glu Val Glu Gly Met Arg Trp Ala Gly Asn		
35	40	45
Ala Asn Glu Leu Asn Ala Arg Tyr Ala Ala Asp Gly Tyr Ala Arg Ile		
50	55	60
Lys Gly Met Ser Cys Ile Ile Thr Thr Phe Gly Val Gly Glu Leu Ser		
65	70	75
		80

Ala Leu Asn Gly Ile Ala Gly Ser Tyr Ala Glu His Val Gly Val Leu
 85 90 95
 His Val Val Gly Val Pro Ser Ile Ser Ser Gln Ala Lys Gln Leu Leu
 100 105 110
 Leu His His Thr Leu Gly Asn Gly Asp Phe Thr Val Phe His Arg Met
 115 120 125
 Ser Ala Asn Ile Ser Glu Thr Thr Ala Met Ile Thr Asp Ile Cys Thr
 130 135 140
 Ala Pro Ala Glu Ile Asp Arg Cys Ile Arg Thr Thr Tyr Val Thr Gln
 145 150 155 160
 Arg Pro Val Tyr Leu Gly Leu Pro Ala Asn Leu Val Asp Leu Asn Val
 165 170 175
 Pro Ala Lys Leu Leu Gln Thr Pro Ile Asp Met Ser Leu Lys Pro Asn
 180 185 190
 Asp Ala Glu Ser Glu Lys Glu Val Ile Asp Thr Ile Leu Val Leu Ala
 195 200 205
 Lys Asp Ala Lys Asn Pro Val Ile Leu Ala Asp Ala Cys Cys Ser Arg
 210 215 220
 His Asp Val Lys Ala Glu Thr Lys Lys Leu Ile Asp Leu Thr Gln Phe
 225 230 235 240
 Pro Ala Phe Val Thr Pro Met Gly Lys Gly Ser Ile Ser Glu Gln His
 245 250 255
 Pro Arg Tyr Gly Val Tyr Val Gly Thr Leu Ser Lys Pro Glu Val
 260 265 270
 Lys Glu Ala Val Glu Ser Ala Asp Leu Ile Leu Ser Val Gly Ala Leu
 275 280 285
 Leu Ser Asp Phe Asn Thr Gly Ser Phe Ser Tyr Ser Tyr Lys Thr Lys
 290 295 300
 Asn Ile Val Glu Phe His Ser Asp His Met Lys Ile Arg Asn Ala Thr
 305 310 315 320
 Phe Pro Gly Val Gln Met Lys Phe Val Leu Gln Lys Leu Leu Thr Asn
 325 330 335
 Ile Ala Asp Ala Ala Lys Gly Tyr Lys Pro Val Ala Val Pro Ala Arg
 340 345 350
 Thr Pro Ala Asn Ala Ala Val Pro Ala Ser Thr Pro Leu Lys Gln Glu
 355 360 365
 Trp Met Trp Asn Gln Leu Gly Asn Phe Leu Gln Glu Gly Asp Val Val
 370 375 380
 Ile Ala Glu Thr Gly Thr Ser Ala Phe Gly Ile Asn Gln Thr Thr Phe
 385 390 395 400
 Pro Asn Asn Thr Tyr Gly Ile Ser Gln Val Leu Trp Gly Ser Ile Gly
 405 410 415
 Phe Thr Thr Gly Ala Thr Leu Gly Ala Ala Phe Ala Ala Glu Glu Ile
 420 425 430
 Asp Pro Lys Lys Arg Val Ile Leu Phe Ile Gly Asp Gly Ser Leu Gln
 435 440 445
 Leu Thr Val Gln Glu Ile Ser Thr Met Ile Arg Trp Gly Leu Lys Pro
 450 455 460
 Tyr Leu Phe Val Leu Asn Asn Asp Gly Tyr Thr Ile Glu Lys Leu Ile
 465 470 475 480
 His Gly Pro Lys Ala Gln Tyr Asn Glu Ile Gln Gly Trp Asp His Leu
 485 490 495
 Ser Leu Leu Pro Thr Phe Gly Ala Lys Asp Tyr Glu Thr His Arg Val
 500 505 510
 Ala Thr Thr Gly Glu Trp Asp Lys Leu Thr Gln Asp Lys Ser Phe Asn
 515 520 525
 Asp Asn Ser Lys Ile Arg Met Ile Glu Val Met Leu Pro Val Phe Asp

530	535	540
Ala Pro Gln Asn Leu Val Glu Gln Ala Lys Leu Thr Ala Ala Thr Asn		
545	550	555
Ala Lys Gln		560

<210> 14
 <211> 550
 <212> PRT
 <213> *Salmonella typhimurium*

<400> 14		
Met Gln Asn Pro Tyr Thr Val Ala Asp Tyr Leu Leu Asp Arg Leu Ala		
1	5	10
Gly Cys Gly Ile Gly His Leu Phe Gly Val Pro Gly Asp Tyr Asn Leu		
20	25	30
Gln Phe Leu Asp His Val Ile Asp His Pro Thr Leu Arg Trp Val Gly		
35	40	45
Cys Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg		
50	55	60
Met Ser Gly Ala Gly Ala Leu Leu Thr Thr Phe Gly Val Gly Glu Leu		
65	70	75
Ser Ala Ile Asn Gly Ile Ala Gly Ser Tyr Ala Glu Tyr Val Pro Val		
85	90	95
Leu His Ile Val Gly Ala Pro Cys Ser Ala Ala Gln Gln Arg Gly Glu		
100	105	110
Leu Met His His Thr Leu Gly Asp Gly Asp Phe Arg His Phe Tyr Arg		
115	120	125
Met Ser Gln Ala Ile Ser Ala Ala Ser Ala Ile Leu Asp Glu Gln Asn		
130	135	140
Ala Cys Phe Glu Ile Asp Arg Val Leu Gly Glu Met Leu Ala Ala Arg		
145	150	155
Arg Pro Gly Tyr Ile Met Leu Pro Ala Asp Val Ala Lys Lys Thr Ala		
165	170	175
Ile Pro Pro Thr Gln Ala Leu Ala Leu Pro Val His Glu Ala Gln Ser		
180	185	190
Gly Val Glu Thr Ala Phe Arg Tyr His Ala Arg Gln Cys Leu Met Asn		
195	200	205
Ser Arg Arg Ile Ala Leu Leu Ala Asp Phe Leu Ala Gly Arg Phe Gly		
210	215	220
Leu Arg Pro Leu Leu Gln Arg Trp Met Ala Glu Thr Pro Ile Ala His		
225	230	235
Ala Thr Leu Leu Met Gly Lys Gly Leu Phe Asp Glu Gln His Pro Asn		
245	250	255
Phe Val Gly Thr Tyr Ser Ala Gly Ala Ser Ser Lys Glu Val Arg Gln		
260	265	270
Ala Ile Glu Asp Ala Asp Arg Val Ile Cys Val Gly Thr Arg Phe Val		
275	280	285
Asp Thr Leu Thr Ala Gly Phe Thr Gln Gln Leu Pro Ala Glu Arg Thr		
290	295	300
Leu Glu Ile Gln Pro Tyr Ala Ser Arg Ile Gly Glu Thr Trp Phe Asn		
305	310	315
Leu Pro Met Ala Gln Ala Val Ser Thr Leu Arg Glu Leu Cys Leu Glu		
325	330	335
Cys Ala Phe Ala Pro Pro Pro Thr Arg Ser Ala Gly Gln Pro Val Arg		
340	345	350

Ile	Asp	Lys	Gly	Glu	Leu	Thr	Gln	Glu	Ser	Phe	Trp	Gln	Thr	Leu	Gln
355				360								365			
Gln	Tyr	Leu	Lys	Pro	Gly	Asp	Ile	Ile	Leu	Val	Asp	Gln	Gly	Thr	Ala
370				375								380			
Ala	Phe	Gly	Ala	Ala	Ala	Leu	Ser	Leu	Pro	Asp	Gly	Ala	Glu	Val	Val
385				390							395			400	
Leu	Gln	Pro	Leu	Trp	Gly	Ser	Ile	Gly	Tyr	Ser	Leu	Pro	Ala	Ala	Phe
				405					410				415		
Gly	Ala	Gln	Thr	Ala	Cys	Pro	Asp	Arg	Arg	Val	Ile	Leu	Ile	Ile	Gly
				420				425				430			
Asp	Gly	Ala	Ala	Gln	Leu	Thr	Ile	Gln	Glu	Met	Gly	Ser	Met	Leu	Arg
				435				440				445			
Asp	Gly	Gln	Ala	Pro	Val	Ile	Leu	Leu	Asn	Asn	Asp	Gly	Tyr	Thr	
				450			455				460				
Val	Glu	Arg	Ala	Ile	His	Gly	Ala	Ala	Gln	Arg	Tyr	Asn	Asp	Ile	Ala
465				470				475						480	
Ser	Trp	Asn	Trp	Thr	Gln	Ile	Pro	Pro	Ala	Leu	Asn	Ala	Ala	Gln	Gln
				485				490				495			
Ala	Glu	Cys	Trp	Arg	Val	Thr	Gln	Ala	Ile	Gln	Leu	Ala	Glu	Val	Leu
				500				505				510			
Glu	Arg	Leu	Ala	Arg	Pro	Gln	Arg	Leu	Ser	Phe	Ile	Glu	Val	Met	Leu
				515				520				525			
Pro	Lys	Ala	Asp	Leu	Pro	Glu	Leu	Leu	Arg	Thr	Val	Thr	Arg	Ala	Leu
				530			535				540				
Glu	Ala	Arg	Asn	Gly	Gly										
			545		550										

<210> 15
<211> 568
<212> PRT
<213> Zymomonas mobilis

<400> 15															
Met	Ser	Tyr	Thr	Val	Gly	Thr	Tyr	Leu	Ala	Glu	Arg	Leu	Val	Gln	Ile
1								5			10				15
Gly	Leu	Lys	His	His	Phe	Ala	Val	Ala	Gly	Asp	Tyr	Asn	Leu	Val	Leu
								20			25				30
Leu	Asp	Asn	Leu	Leu	Asn	Lys	Asn	Met	Glu	Gln	Val	Tyr	Cys	Cys	
								35			40				45
Asn	Glu	Leu	Asn	Cys	Gly	Phe	Ser	Ala	Glu	Gly	Tyr	Ala	Arg	Ala	Lys
								50			55				60
Gly	Ala	Ala	Ala	Ala	Val	Val	Thr	Tyr	Ser	Val	Gly	Ala	His	Ser	Ala
								65			70				80
Phe	Asp	Ala	Ile	Gly	Gly	Ala	Tyr	Ala	Glu	Asn	Leu	Pro	Val	Ile	Leu
								85			90				95
Ile	Ser	Gly	Ala	Pro	Asn	Asn	Asn	Asp	His	Ala	Ala	Gly	His	Val	Leu
								100			105				110
His	His	Ala	Leu	Gly	Lys	Thr	Asp	Tyr	His	Tyr	Gln	Leu	Glu	Met	Ala
								115			120				125
Lys	Asn	Ile	Thr	Ala	Ala	Ala	Glu	Ala	Ile	Tyr	Thr	Pro	Glu	Glu	Ala
								130			135				140
Pro	Ala	Lys	Ile	Asp	His	Val	Ile	Lys	Thr	Ala	Leu	Ala	Lys	Lys	
								145			150				160
Pro	Val	Tyr	Leu	Glu	Ile	Ala	Cys	Asn	Ile	Ala	Ser	Met	Pro	Cys	Ala
								165			170				175
Ala	Pro	Gly	Pro	Ala	Ser	Ala	Leu	Phe	Asn	Asp	Glu	Ala	Ser	Asp	Glu

	180	185	190
Ala Ser Leu Asn Ala Ala Val Asp Glu Thr Leu Lys Phe Ile Ala Asn			
195	200	205	
Arg Asp Lys Val Ala Val Leu Val Gly Ser Lys Leu Arg Ala Ala Gly			
210	215	220	
Ala Glu Glu Ala Ala Val Lys Phe Thr Asp Ala Leu Gly Gly Ala Val			
225	230	235	240
Ala Thr Met Ala Ala Lys Ser Phe Phe Pro Glu Glu Asn Pro His			
245	250	255	
Tyr Ile Gly Thr Ser Trp Gly Glu Val Ser Tyr Pro Gly Val Glu Lys			
260	265	270	
Thr Met Lys Glu Ala Asp Ala Val Ile Ala Leu Ala Pro Val Phe Asn			
275	280	285	
Asp Tyr Ser Thr Thr Gly Trp Thr Asp Ile Pro Asp Pro Lys Lys Leu			
290	295	300	
Val Leu Ala Glu Pro Arg Ser Val Val Val Arg Arg Ile Arg Phe Pro			
305	310	315	320
Ser Val His Leu Lys Asp Tyr Leu Thr Arg Leu Ala Gln Lys Val Ser			
325	330	335	
Lys Lys Thr Gly Ser Leu Asp Phe Phe Lys Ser Leu Asn Ala Gly Glu			
340	345	350	
Leu Lys Lys Ala Ala Pro Ala Asp Pro Ser Ala Pro Leu Val Asn Ala			
355	360	365	
Glu Ile Ala Arg Gln Val Glu Ala Leu Leu Thr Pro Asn Thr Thr Val			
370	375	380	
Ile Ala Glu Thr Gly Asp Ser Trp Phe Asn Ala Gln Arg Met Lys Leu			
385	390	395	400
Pro Asn Gly Ala Arg Val Glu Tyr Glu Met Gln Trp Gly His Ile Gly			
405	410	415	
Trp Ser Val Pro Ala Ala Phe Gly Tyr Ala Val Gly Ala Pro Glu Arg			
420	425	430	
Arg Asn Ile Leu Met Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln			
435	440	445	
Glu Val Ala Gln Met Val Arg Leu Lys Leu Pro Val Ile Ile Phe Leu			
450	455	460	
Ile Asn Asn Tyr Gly Tyr Thr Ile Glu Val Met Ile His Asp Gly Pro			
465	470	475	480
Tyr Asn Asn Ile Lys Asn Trp Asp Tyr Ala Gly Leu Met Glu Val Phe			
485	490	495	
Asn Gly Asn Gly Gly Tyr Asp Ser Gly Ala Ala Lys Gly Leu Lys Ala			
500	505	510	
Lys Thr Gly Gly Glu Leu Ala Glu Ala Ile Lys Val Ala Leu Ala Asn			
515	520	525	
Thr Asp Gly Pro Thr Leu Ile Glu Cys Phe Ile Gly Arg Glu Asp Cys			
530	535	540	
Thr Glu Glu Leu Val Lys Trp Gly Lys Arg Val Ala Ala Ala Asn Ser			
545	550	555	560
Arg Lys Pro Val Asn Lys Leu Leu			
565			

<210> 16
<211> 687
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 16

Met Ile Arg Gln Ser Thr Leu Lys Asn Phe Ala Ile Lys Arg Cys Phe
 1 5 10 15
 Gln His Ile Ala Tyr Arg Asn Thr Pro Ala Met Arg Ser Val Ala Leu
 20 25 30
 Ala Gln Arg Phe Tyr Ser Ser Ser Arg Tyr Tyr Ser Ala Ser Pro
 35 40 45
 Leu Pro Ala Ser Lys Arg Pro Glu Pro Ala Pro Ser Phe Asn Val Asp
 50 55 60
 Pro Leu Glu Gln Pro Ala Glu Pro Ser Lys Leu Ala Lys Lys Leu Arg
 65 70 75 80
 Ala Glu Pro Asp Met Asp Thr Ser Phe Val Gly Leu Thr Gly Gly Gln
 85 90 95
 Ile Phe Asn Glu Met Met Ser Arg Gln Asn Val Asp Thr Val Phe Gly
 100 105 110
 Tyr Pro Gly Gly Ala Ile Leu Pro Val Tyr Asp Ala Ile His Asn Ser
 115 120 125
 Asp Lys Phe Asn Phe Val Leu Pro Lys His Glu Gln Gly Ala Gly His
 130 135 140
 Met Ala Glu Gly Tyr Ala Arg Ala Ser Gly Lys Pro Gly Val Val Leu
 145 150 155 160
 Val Thr Ser Gly Pro Gly Ala Thr Asn Val Val Thr Pro Met Ala Asp
 165 170 175
 Ala Phe Ala Asp Gly Ile Pro Met Val Val Phe Thr Gly Gln Val Pro
 180 185 190
 Thr Ser Ala Ile Gly Thr Asp Ala Phe Gln Glu Ala Asp Val Val Gly
 195 200 205
 Ile Ser Arg Ser Cys Thr Lys Trp Asn Val Met Val Lys Ser Val Glu
 210 215 220
 Glu Leu Pro Leu Arg Ile Asn Glu Ala Phe Glu Ile Ala Thr Ser Gly
 225 230 235 240
 Arg Pro Gly Pro Val Leu Val Asp Leu Pro Lys Asp Val Thr Ala Ala
 245 250 255
 Ile Leu Arg Asn Pro Ile Pro Thr Lys Thr Thr Leu Pro Ser Asn Ala
 260 265 270
 Leu Asn Gln Leu Thr Ser Arg Ala Gln Asp Glu Phe Val Met Gln Ser
 275 280 285
 Ile Asn Lys Ala Ala Asp Leu Ile Asn Leu Ala Lys Lys Pro Val Leu
 290 295 300
 Tyr Val Gly Ala Gly Ile Leu Asn His Ala Asp Gly Pro Arg Leu Leu
 305 310 315 320
 Lys Glu Leu Ser Asp Arg Ala Gln Ile Pro Val Thr Thr Leu Gln
 325 330 335
 Gly Leu Gly Ser Phe Asp Gln Glu Asp Pro Lys Ser Leu Asp Met Leu
 340 345 350
 Gly Met His Gly Cys Ala Thr Ala Asn Leu Ala Val Gln Asn Ala Asp
 355 360 365
 Leu Ile Ile Ala Val Gly Ala Arg Phe Asp Asp Arg Val Thr Gly Asn
 370 375 380
 Ile Ser Lys Phe Ala Pro Glu Ala Arg Arg Ala Ala Glu Gly Arg
 385 390 395 400
 Gly Gly Ile Ile His Phe Glu Val Ser Pro Lys Asn Ile Asn Lys Val
 405 410 415
 Val Gln Thr Gln Ile Ala Val Glu Gly Asp Ala Thr Thr Asn Leu Gly
 420 425 430
 Lys Met Met Ser Lys Ile Phe Pro Val Lys Glu Arg Ser Glu Trp Phe
 435 440 445
 Ala Gln Ile Asn Lys Trp Lys Lys Glu Tyr Pro Tyr Ala Tyr Met Glu

450	455	460
Glu Thr Pro Gly Ser Lys Ile Lys Pro Gln Thr Val Ile Lys Lys Leu		
465	470	475
Ser Lys Val Ala Asn Asp Thr Gly Arg His Val Ile Val Thr Thr Gly		480
485	490	495
Val Gly Gln His Gln Met Trp Ala Ala Gln His Trp Thr Trp Arg Asn		
500	505	510
Pro His Thr Phe Ile Thr Ser Gly Gly Leu Gly Thr Met Gly Tyr Gly		
515	520	525
Leu Pro Ala Ala Ile Gly Ala Gln Val Ala Lys Pro Glu Ser Leu Val		
530	535	540
Ile Asp Ile Asp Gly Asp Ala Ser Phe Asn Met Thr Leu Thr Glu Leu		
545	550	555
Ser Ser Ala Val Gln Ala Gly Thr Pro Val Lys Ile Leu Ile Leu Asn		560
565	570	575
Asn Glu Glu Gln Gly Met Val Thr Gln Trp Gln Ser Leu Phe Tyr Glu		
580	585	590
His Arg Tyr Ser His Thr His Gln Leu Asn Pro Asp Phe Ile Lys Leu		
595	600	605
Ala Glu Ala Met Gly Leu Lys Gly Leu Arg Val Lys Lys Gln Glu Glu		
610	615	620
Leu Asp Ala Lys Leu Lys Glu Phe Val Ser Thr Lys Gly Pro Val Leu		
625	630	635
Leu Glu Val Glu Val Asp Lys Lys Val Pro Val Leu Pro Met Val Ala		640
645	650	655
Gly Gly Ser Gly Leu Asp Glu Phe Ile Asn Phe Asp Pro Glu Val Glu		
660	665	670
Arg Gln Gln Thr Glu Leu Arg His Lys Arg Thr Gly Gly Lys His		
675	680	685

<210> 17
<211> 686
<212> PRT
<213> Magnaporthe grisea

<400> 17		
Met Leu Arg Thr Val Gly Arg Lys Ala Leu Arg Gly Ser Ser Lys Gly		
1	5	10
Cys Ser Arg Thr Ile Ser Thr Leu Lys Pro Ala Thr Ala Thr Ile Ala		15
20	25	30
Lys Pro Gly Ser Arg Thr Leu Ser Thr Pro Ala Thr Ala Thr Ala Thr		
35	40	45
Ala Pro Arg Thr Lys Pro Ser Ala Ser Phe Asn Ala Arg Arg Asp Pro		
50	55	60
Gln Pro Leu Val Asn Pro Arg Ser Gly Glu Ala Asp Glu Ser Phe Ile		
65	70	75
Gly Lys Thr Gly Gly Glu Ile Phe His Glu Met Met Leu Arg Gln Asn		80
85	90	95
Val Lys His Ile Phe Gly Tyr Pro Gly Gly Ala Ile Leu Pro Val Phe		
100	105	110
Asp Ala Ile Tyr Asn Ser Lys His Ile Asp Phe Val Leu Pro Lys His		
115	120	125
Glu Gln Gly Ala Gly His Met Ala Glu Gly Tyr Ala Arg Ala Ser Gly		
130	135	140
Lys Pro Gly Val Val Leu Val Thr Ser Gly Pro Gly Ala Thr Asn Val		
145	150	155
		160

Ile Thr Pro Met Ala Asp Ala Leu Ala Asp Gly Thr Pro Leu Val Val
 165 170 175
 Phe Ser Gly Gln Val Val Thr Ser Asp Ile Gly Ser Asp Ala Phe Gln
 180 185 190
 Glu Ala Asp Val Ile Gly Ile Ser Arg Ser Cys Thr Lys Trp Asn Val
 195 200 205
 Met Val Lys Ser Ala Asp Glu Leu Pro Arg Arg Ile Asn Glu Ala Phe
 210 215 220
 Glu Ile Ala Thr Ser Gly Arg Pro Gly Pro Val Leu Val Asp Pro Ala
 225 230 235 240
 Lys Asp Val Thr Ala Ser Val Leu Arg Arg Ala Ile Pro Thr Glu Thr
 245 250 255
 Ser Ile Pro Ser Ile Ser Ala Ala Arg Ala Val Gln Glu Ala Gly
 260 265 270
 Arg Lys Gln Leu Glu His Ser Ile Lys Arg Val Ala Asp Leu Val Asn
 275 280 285
 Ile Ala Lys Lys Pro Val Ile Tyr Ala Gly Gln Gly Val Ile Leu Ser
 290 295 300
 Glu Gly Gly Val Glu Leu Leu Lys Ala Leu Ala Asp Lys Ala Ser Ile
 305 310 315 320
 Pro Val Thr Thr Leu His Gly Leu Gly Ala Phe Asp Glu Leu Asp
 325 330 335
 Glu Lys Ala Leu His Met Leu Gly Met His Gly Ser Ala Tyr Ala Asn
 340 345 350
 Met Ser Met Gln Glu Ala Asp Leu Ile Ile Ala Leu Gly Gly Arg Phe
 355 360 365
 Asp Asp Arg Val Thr Gly Ser Ile Pro Lys Phe Ala Pro Ala Ala Lys
 370 375 380
 Leu Ala Ala Ala Glu Gly Arg Gly Gly Ile Val His Phe Glu Ile Met
 385 390 395 400
 Pro Lys Asn Ile Asn Lys Val Val Gln Ala Thr Glu Ala Ile Glu Gly
 405 410 415
 Asp Val Ala Ser Asn Leu Lys Leu Leu Pro Lys Ile Glu Gln Arg
 420 425 430
 Ser Met Thr Asp Arg Lys Glu Trp Phe Asp Gln Ile Lys Glu Trp Lys
 435 440 445
 Glu Lys Trp Pro Leu Ser His Tyr Glu Arg Ala Glu Arg Ser Gly Leu
 450 455 460
 Ile Lys Pro Gln Thr Leu Ile Glu Glu Leu Ser Asn Leu Thr Ala Asp
 465 470 475 480
 Arg Lys Asp Met Thr Tyr Ile Thr Thr Gly Val Gly Gln His Gln Met
 485 490 495
 Trp Thr Ala Gln His Phe Arg Trp Arg His Pro Arg Ser Met Ile Thr
 500 505 510
 Ser Gly Gly Leu Gly Thr Met Gly Tyr Gly Leu Pro Ala Ala Ile Gly
 515 520 525
 Ala Lys Val Ala Arg Pro Asp Ala Leu Val Ile Asp Ile Asp Gly Asp
 530 535 540
 Ala Ser Phe Asn Met Thr Leu Thr Glu Leu Ser Thr Ala Ala Gln Phe
 545 550 555 560
 Asn Ile Gly Val Lys Val Ile Val Leu Asn Asn Glu Glu Gln Gly Met
 565 570 575
 Val Thr Gln Trp Gln Asn Leu Phe Tyr Glu Asp Arg Tyr Ser His Thr
 580 585 590
 His Gln Arg Asn Pro Asp Phe Met Lys Leu Ala Asp Ala Met Asp Val
 595 600 605
 Gln His Arg Arg Val Ser Lys Pro Asp Asp Val Gly Asp Ala Leu Thr

610	615	620
Trp Leu Ile Asn Thr Asp Gly Pro Ala Leu Leu Glu Val Met Thr Asp		
625	630	635
Lys Lys Val Pro Val Leu Pro Met Val Pro Gly Gly Asn Gly Leu His		640
645	650	655
Glu Phe Ile Thr Phe Asp Ala Ser Lys Asp Lys Gln Arg Arg Glu Leu		
660	665	670
Met Arg Ala Arg Thr Asn Gly Leu His Gly Arg Thr Ala Val		
675	680	685

<210> 18
<211> 1728
<212> DNA
<213> Unknown

<220>
<223> Fungal isolate from soil sample

<221> CDS
<222> (1)...(1728)

<400> 18				
atg gcc agc atc aac atc agg gtg cag aat ctc gag caa ccc atg gac				48
Met Ala Ser Ile Asn Ile Arg Val Gln Asn Leu Glu Gln Pro Met Asp				
1	5	10	15	
gtt gcc gag tat ctt ttc cgg cgt ctc cac gaa atc ggc att cgc tcc				96
Val Ala Glu Tyr Leu Phe Arg Arg Leu His Glu Ile Gly Ile Arg Ser				
20	25	30		
atc cac ggt ctt cca ggc gat tac aac cct ctt gcc ctc gac tat ttg				144
Ile His Gly Leu Pro Gly Asp Tyr Asn Pro Leu Ala Leu Asp Tyr Leu				
35	40	45		
cca tca tgt ggc ctg aga tgg gtt ggc agc gtc aac gaa ctc aat gct				192
Pro Ser Cys Gly Leu Arg Trp Val Gly Ser Val Asn Glu Leu Asn Ala				
50	55	60		
gct tat gct gat ggc tat gcc cgc gtc aag cag atg gga gct ctc				240
Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Val Lys Gln Met Gly Ala Leu				
65	70	75	80	
atc acc act ttt gga gtg gga gag ctc tca gcc atc aat ggc gtt gcc				288
Ile Thr Thr Phe Gly Val Gly Glu Leu Ser Ala Ile Asn Gly Val Ala				
85	90	95		
ggt gcc ttt tcg gaa cac gtc cca gtc gtt cac att gtt ggc tgc cct				336
Gly Ala Phe Ser Glu His Val Pro Val Val His Ile Val Gly Cys Pro				
100	105	110		
tcc act gcc tcg cag cga aac ggc atg ctc ctc cac cac acg ctt gga				384
Ser Thr Ala Ser Gln Arg Asn Gly Met Leu Leu His His Thr Leu Gly				
115	120	125		
aac ggc gac ttc aac atc ttt gcc aac atg agc gct caa atc tct tgc				432
Asn Gly Asp Phe Asn Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys				

130	135	140	
gaa gtg gcc aag ctc acc aac cct gcc gaa att gcg acc cag atc gac Glu Val Ala Lys Leu Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp	145	150	480
	155	160	
cat gcc ctc cgc gtt tgc ttc att cgt tct cgg ccc gtc tac atc atg His Ala Leu Arg Val Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met	165	170	528
		175	
ctt ccc acc gat atg gtc cag gcc aaa gta gaa ggt gcc aga ctc aag Leu Pro Thr Asp Met Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys	180	185	576
		190	
gaa cca att gac ttg tcg gag cct cca aat gat ccc gag aaa gaa gca Glu Pro Ile Asp Leu Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala	195	200	624
		205	
tac gtc gtt gac gtt gtc ctc aag tac ctc cgt gct gca aag aac ccc Tyr Val Val Asp Val Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro	210	215	672
		220	
gtc atc ctt gtc gat gct tgt gct atc cgt cat cgt gtt ctt gat gag Val Ile Leu Val Asp Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu	225	230	720
		235	240
gtt cat gat ctc atc gaa aag aca aac ctc ccc gtc ttt gtc act cct Val His Asp Leu Ile Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro	245	250	768
		255	
atg ggc aaa ggt gct gtt aac gaa gaa cac ccg aca tat ggt ggt gtc Met Gly Lys Gly Ala Val Asn Glu Glu His Pro Thr Tyr Gly Gly Val	260	265	816
		270	
tat gcc ggt gac ggc tca cat ccg cct caa gtt aag gac atg gtt gag Tyr Ala Gly Asp Gly Ser His Pro Pro Gln Val Lys Asp Met Val Glu	275	280	864
		285	
tct tct gat ttg ata ttg aca atc ggt gct ctc aag agc gac ttc aac Ser Ser Asp Leu Ile Leu Thr Ile Gly Ala Leu Lys Ser Asp Phe Asn	290	295	912
		300	
act gct ggc ttc tct tac cgt acc tca cag ctg aac acg att gat cta Thr Ala Gly Phe Ser Tyr Arg Thr Ser Gln Leu Asn Thr Ile Asp Leu	305	310	960
		315	320
cac agc gac cac tgc att gtc aaa tac tcg aca tat cca ggt gtc cag His Ser Asp His Cys Ile Val Lys Tyr Ser Thr Tyr Pro Gly Val Gln	325	330	1008
		335	
atg agg ggt gtg ctg cga caa gtg att aag cag ctc gat gca tct gag Met Arg Gly Val Leu Arg Gln Val Ile Lys Gln Leu Asp Ala Ser Glu	340	345	1056
		350	
atc aac gct cag cca gcg cca gtc gtc gag aat gaa gtt gcc aaa aac Ile Asn Ala Gln Pro Ala Pro Val Val Glu Asn Glu Val Ala Lys Asn	355	360	1104
		365	

cga gat aac tca ccc gtc att aca caa gct ttc ttc tgg ccg cgc gtg		1152	
Arg Asp Asn Ser Pro Val Ile Thr Gln Ala Phe Phe Trp Pro Arg Val			
370	375	380	
gga gag ttc ctg aag aag aac gac atc gtc att acc gag act gga aca		1200	
Gly Glu Phe Leu Lys Lys Asn Asp Ile Val Ile Thr Glu Thr Gly Thr			
385	390	395	400
gcc aac ttt ggc atc tgg gat act aag ttt ccc tct ggc gtt act gcg		1248	
Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe Pro Ser Gly Val Thr Ala			
405	410	415	
ctt tct cag gtc ctt tgg gga agc att ggt tgg tcc gtt ggt gcc tgc		1296	
Leu Ser Gln Val Leu Trp Gly Ser Ile Gly Trp Ser Val Gly Ala Cys			
420	425	430	
caa gga gcc gtt ctt gca gcc gat gac aac agc gat cgc aga act		1344	
Gln Gly Ala Val Leu Ala Ala Ala Asp Asp Asn Ser Asp Arg Arg Thr			
435	440	445	
atc ctc ttt gtt ggt gat ggc tca ttc cag ctc act gct caa gaa ttg		1392	
Ile Leu Phe Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Leu			
450	455	460	
agc aca atg att cgt ctc aag ctg aag ccc atc atc ttt gtc atc tgc		1440	
Ser Thr Met Ile Arg Leu Lys Leu Lys Pro Ile Ile Phe Val Ile Cys			
465	470	475	480
aac gat ggc ttt acc att gaa cga ttc att cac ggc atg gaa gcc gag		1488	
Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile His Gly Met Glu Ala Glu			
485	490	495	
tac aac gac atc gca aat tgg gac ttc aag gct ctg gtt gac gtc ttt		1536	
Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys Ala Leu Val Asp Val Phe			
500	505	510	
ggc ggc tct aag acg gcc aag aag ttc gcc gtc aag acc aag gac gag		1584	
Gly Gly Ser Lys Thr Ala Lys Lys Phe Ala Val Lys Thr Lys Asp Glu			
515	520	525	
ctg gac agc ctt ctc aca gac cct acc ttt aac gcc gca gaa tgc ctc		1632	
Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe Asn Ala Ala Glu Cys Leu			
530	535	540	
cag ttt gtc gag cta tat atg ccc aaa gaa gat gct cct cga gca ttg		1680	
Gln Phe Val Glu Leu Tyr Met Pro Lys Glu Asp Ala Pro Arg Ala Leu			
545	550	555	560
atc atg acg gca gaa gct agc gcg agg aac aat gcc aag aca gag taa		1728	
Ile Met Thr Ala Glu Ala Ser Ala Arg Asn Asn Ala Lys Thr Glu *			
565	570	575	

<210> 19
<211> 575

<212> PRT
<213> Unknown

<220>
<223> Fungal isolate from soil sample

<400> 19
Met Ala Ser Ile Asn Ile Arg Val Gln Asn Leu Glu Gln Pro Met Asp
1 5 10 15
Val Ala Glu Tyr Leu Phe Arg Arg Leu His Glu Ile Gly Ile Arg Ser
20 25 30
Ile His Gly Leu Pro Gly Asp Tyr Asn Pro Leu Ala Leu Asp Tyr Leu
35 40 45
Pro Ser Cys Gly Leu Arg Trp Val Gly Ser Val Asn Glu Leu Asn Ala
50 55 60
Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Val Lys Gln Met Gly Ala Leu
65 70 75 80
Ile Thr Thr Phe Gly Val Gly Glu Leu Ser Ala Ile Asn Gly Val Ala
85 90 95
Gly Ala Phe Ser Glu His Val Pro Val Val His Ile Val Gly Cys Pro
100 105 110
Ser Thr Ala Ser Gln Arg Asn Gly Met Leu Leu His His Thr Leu Gly
115 120 125
Asn Gly Asp Phe Asn Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys
130 135 140
Glu Val Ala Lys Leu Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp
145 150 155 160
His Ala Leu Arg Val Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met
165 170 175
Leu Pro Thr Asp Met Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys
180 185 190
Glu Pro Ile Asp Leu Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala
195 200 205
Tyr Val Val Asp Val Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro
210 215 220
Val Ile Leu Val Asp Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu
225 230 235 240
Val His Asp Leu Ile Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro
245 250 255
Met Gly Lys Gly Ala Val Asn Glu Glu His Pro Thr Tyr Gly Gly Val
260 265 270
Tyr Ala Gly Asp Gly Ser His Pro Pro Gln Val Lys Asp Met Val Glu
275 280 285
Ser Ser Asp Leu Ile Leu Thr Ile Gly Ala Leu Lys Ser Asp Phe Asn
290 295 300
Thr Ala Gly Phe Ser Tyr Arg Thr Ser Gln Leu Asn Thr Ile Asp Leu
305 310 315 320
His Ser Asp His Cys Ile Val Lys Tyr Ser Thr Tyr Pro Gly Val Gln
325 330 335
Met Arg Gly Val Leu Arg Gln Val Ile Lys Gln Leu Asp Ala Ser Glu
340 345 350
Ile Asn Ala Gln Pro Ala Pro Val Val Glu Asn Glu Val Ala Lys Asn
355 360 365
Arg Asp Asn Ser Pro Val Ile Thr Gln Ala Phe Phe Trp Pro Arg Val
370 375 380
Gly Glu Phe Leu Lys Lys Asn Asp Ile Val Ile Thr Glu Thr Gly Thr
385 390 395 400

Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe Pro Ser Gly Val Thr Ala
 405 410 415
 Leu Ser Gln Val Leu Trp Gly Ser Ile Gly Trp Ser Val Gly Ala Cys
 420 425 430
 Gln Gly Ala Val Leu Ala Ala Asp Asp Asn Ser Asp Arg Arg Thr
 435 440 445
 Ile Leu Phe Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Leu
 450 455 460
 Ser Thr Met Ile Arg Leu Lys Leu Lys Pro Ile Ile Phe Val Ile Cys
 465 470 475 480
 Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile His Gly Met Glu Ala Glu
 485 490 495
 Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys Ala Leu Val Asp Val Phe
 500 505 510
 Gly Gly Ser Lys Thr Ala Lys Lys Phe Ala Val Lys Thr Lys Asp Glu
 515 520 525
 Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe Asn Ala Ala Glu Cys Leu
 530 535 540
 Gln Phe Val Glu Leu Tyr Met Pro Lys Glu Asp Ala Pro Arg Ala Leu
 545 550 555 560
 Ile Met Thr Ala Glu Ala Ser Ala Arg Asn Asn Ala Lys Thr Glu
 565 570 575

<210> 20
 <211> 1728
 <212> DNA
 <213> Unknown

<220>
 <223> Fungal isolate from soil sample

<221> CDS
 <222> (1)...(1728)

<400> 20
 atg gcc agc atc aac atc agg gtg cag aat ctc gag caa ccc atg gac 48
 Met Ala Ser Ile Asn Ile Arg Val Gln Asn Leu Glu Gln Pro Met Asp
 1 5 10 15

 gtt gcc gag tat ctt ttc cgg cgt ctc cac gaa atc ggc att cgc tcc 96
 Val Ala Glu Tyr Leu Phe Arg Arg Leu His Glu Ile Gly Ile Arg Ser
 20 25 30

 atc cac ggt ctt cca ggc gat tac aac ctt ctt gcc ctc gac tat ttg 144
 Ile His Gly Leu Pro Gly Asp Tyr Asn Leu Leu Ala Leu Asp Tyr Leu
 35 40 45

 cca tca tgt ggc ctg aga tgg gtt ggc agc gtc aac gaa ctc aat gct 192
 Pro Ser Cys Gly Leu Arg Trp Val Gly Ser Val Asn Glu Leu Asn Ala
 50 55 60

 gct tat gct gct gat ggc tat gcc cgc gtc aag cag atg gga gct ctc 240
 Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Val Lys Gln Met Gly Ala Leu
 65 70 75 80

 atc acc act ttt gga gtg gga gag ctc tca gcc atc aat ggc gtt gcc 288

Ile Thr Thr Phe Gly Val Gly Glu Leu Ser Ala Ile Asn Gly Val Ala			
85	90	95	
ggt gcc ttt tcg gaa cac gtc cca gtc gtt cac att gtt ggc tgc cct			336
Gly Ala Phe Ser Glu His Val Pro Val Val His Ile Val Gly Cys Pro			
100	105	110	
tcc act gcc tcg cag cga aac ggc atg ctc ctc cac cac acg ctt gga			384
Ser Thr Ala Ser Gln Arg Asn Gly Met Leu Leu His His Thr Leu Gly			
115	120	125	
aac ggc gac ttc aac atc ttt gcc aac atg agc gct caa atc tct tgc			432
Asn Gly Asp Phe Asn Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys			
130	135	140	
gaa gtg gcc aag ctc acc aac cct gcc gaa att gcg acc cag atc gac			480
Glu Val Ala Lys Leu Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp			
145	150	155	160
cat gcc ctc cgc gtt tgc ttc att cgt tct cgg ccc gtc tac atc atg			528
His Ala Leu Arg Val Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met			
165	170	175	
ctt ccc acc gat atg gtc cag gcc aaa gta gaa ggt gcc aga ctc aag			576
Leu Pro Thr Asp Met Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys			
180	185	190	
gaa cca att gac ttg tcg gag cct cca aat gat ccc gag aaa gaa gca			624
Glu Pro Ile Asp Leu Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala			
195	200	205	
tac gtc gtt gac gtc ctc aag tac ctc cgt gct gca aag aac ccc			672
Tyr Val Val Asp Val Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro			
210	215	220	
gtc atc ctt gtc gat gct tgt gct atc cgt cat cgt gtt ctt gat gag			720
Val Ile Leu Val Asp Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu			
225	230	235	240
gtt cat gat ctc atc gaa aag aca aac ctc ccc gtc ttt gtc act cct			768
Val His Asp Leu Ile Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro			
245	250	255	
atg ggc aaa ggt gct gtt aac gaa gaa cac ccg aca tat ggt ggt gtc			816
Met Gly Lys Gly Ala Val Asn Glu Glu His Pro Thr Tyr Gly Gly Val			
260	265	270	
tat gcc ggt gac ggc tca cat ccg cct caa gtt aag gac atg gtt gag			864
Tyr Ala Gly Asp Gly Ser His Pro Pro Gln Val Lys Asp Met Val Glu			
275	280	285	
tct tct gat ttg ata ttg aca atc ggt gct ctc aag agc gac ttc aac			912
Ser Ser Asp Leu Ile Leu Thr Ile Gly Ala Leu Lys Ser Asp Phe Asn			
290	295	300	
act gct ggc ttc tct tac cgt acc tca cag ctg aac acg att gat cta			960
Thr Ala Gly Phe Ser Tyr Arg Thr Ser Gln Leu Asn Thr Ile Asp Leu			

305	310	315	320	
cac agc gac cac tgc att gtc aaa tac tcg aca tat cca ggt gtc cag His Ser Asp His Cys Ile Val Lys Tyr Ser Thr Tyr Pro Gly Val Gln 325		330	335	1008
atg agg ggt gtg ctg cga caa gtg att aag cag ctc gat gca tct gag Met Arg Gly Val Leu Arg Gln Val Ile Lys Gln Leu Asp Ala Ser Glu 340	345	350		1056
atc aac gct cag cca gcg cca gtc gtc gag aat gaa gtt gcc aaa aac Ile Asn Ala Gln Pro Ala Pro Val Val Glu Asn Glu Val Ala Lys Asn 355	360	365		1104
cga gat aac tca ccc gtc att aca caa gct ttc ttc tgg ccg cgc gtg Arg Asp Asn Ser Pro Val Ile Thr Gln Ala Phe Phe Trp Pro Arg Val 370	375	380		1152
gga gag ttc ctg aag aag aac gac atc gtc att acc gag act gga aca Gly Glu Phe Leu Lys Lys Asn Asp Ile Val Ile Thr Glu Thr Gly Thr 385	390	395	400	1200
gcc aac ttt ggc atc tgg gat act aag ttt ccc tct ggc gtt act gcg Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe Pro Ser Gly Val Thr Ala 405	410		415	1248
ctt tct cag gtc ctt tgg gga agc att ggt tgg tcc gtt ggt gcc tgc Leu Ser Gln Val Leu Trp Gly Ser Ile Gly Trp Ser Val Gly Ala Cys 420	425		430	1296
caa gga gcc gtt ctt gca gcc gat gac aac agc gat cgc aga act Gln Gly Ala Val Leu Ala Ala Asp Asp Asn Ser Asp Arg Arg Thr 435	440	445		1344
atc ctc ttt gtt ggt gat ggc tca ttc cag ctc act gct caa gaa ttg Ile Leu Phe Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Leu 450	455	460		1392
agc aca atg att cgt ctc aag ctg aag ccc atc atc ttt gtc atc tgc Ser Thr Met Ile Arg Leu Lys Leu Lys Pro Ile Ile Phe Val Ile Cys 465	470	475	480	1440
aac gat ggc ttt acc att gaa cga ttc att cac ggc atg gaa gcc gag Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile His Gly Met Glu Ala Glu 485	490		495	1488
tac aac gac atc gca aat tgg gac ttc aag gct ctg gtt gac gtc ttt Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys Ala Leu Val Asp Val Phe 500	505		510	1536
ggc ggc tct aag acg gcc aag aag ttc gcc gtc aag acc aag gac gag Gly Gly Ser Lys Thr Ala Lys Lys Phe Ala Val Lys Thr Lys Asp Glu 515	520	525		1584
ctg gac agc ctt ctc aca gac cct acc ttt aac gcc gca gaa tgc ctc Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe Asn Ala Ala Glu Cys Leu 530	535	540		1632

cag ttt gtc gag cta tat atg ccc aaa gaa gat gct cct cga gca ttg 1680
Gln Phe Val Glu Leu Tyr Met Pro Lys Glu Asp Ala Pro Arg Ala Leu
545 550 555 560

atc atg acg gca gaa gct agc gcg agg aac aat gcc aag aca gag taa 1728
Ile Met Thr Ala Glu Ala Ser Ala Arg Asn Asn Ala Lys Thr Glu *
565 570 575

<210> 21
<211> 575
<212> PRT
<213> Unknown

<220>
<223> Fungal isolate from soil sample

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Met Ala Ser Ile Asn Ile Arg Val Gln Asn Leu Glu Gln Pro Met Asp
1 5 10 15
Val Ala Glu Tyr Leu Phe Arg Arg Leu His Glu Ile Gly Ile Arg Ser
20 25 30
Ile His Gly Leu Pro Gly Asp Tyr Asn Leu Leu Ala Leu Asp Tyr Leu
35 40 45
Pro Ser Cys Gly Leu Arg Trp Val Gly Ser Val Asn Glu Leu Asn Ala
50 55 60
Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Val Lys Gln Met Gly Ala Leu
65 70 75 80
Ile Thr Thr Phe Gly Val Gly Glu Leu Ser Ala Ile Asn Gly Val Ala
85 90 95
Gly Ala Phe Ser Glu His Val Pro Val Val His Ile Val Gly Cys Pro
100 105 110
Ser Thr Ala Ser Gln Arg Asn Gly Met Leu Leu His His Thr Leu Gly
115 120 125
Asn Gly Asp Phe Asn Ile Phe Ala Asn Met Ser Ala Gln Ile Ser Cys
130 135 140
Glu Val Ala Lys Leu Thr Asn Pro Ala Glu Ile Ala Thr Gln Ile Asp
145 150 155 160
His Ala Leu Arg Val Cys Phe Ile Arg Ser Arg Pro Val Tyr Ile Met
165 170 175
Leu Pro Thr Asp Met Val Gln Ala Lys Val Glu Gly Ala Arg Leu Lys
180 185 190
Glu Pro Ile Asp Leu Ser Glu Pro Pro Asn Asp Pro Glu Lys Glu Ala
195 200 205
Tyr Val Val Asp Val Val Leu Lys Tyr Leu Arg Ala Ala Lys Asn Pro
210 215 220
Val Ile Leu Val Asp Ala Cys Ala Ile Arg His Arg Val Leu Asp Glu
225 230 235 240
Val His Asp Leu Ile Glu Lys Thr Asn Leu Pro Val Phe Val Thr Pro
245 250 255
Met Gly Lys Gly Ala Val Asn Glu Glu His Pro Thr Tyr Gly Gly Val
260 265 270
Tyr Ala Gly Asp Gly Ser His Pro Pro Gln Val Lys Asp Met Val Glu
275 280 285
Ser Ser Asp Leu Ile Leu Thr Ile Gly Ala Leu Lys Ser Asp Phe Asn

290	295	300
Thr Ala Gly Phe Ser Tyr Arg Thr Ser Gln Leu Asn Thr Ile Asp Leu		
305	310	315
His Ser Asp His Cys Ile Val Lys Tyr Ser Thr Tyr Pro Gly Val Gln		320
325	330	335
Met Arg Gly Val Leu Arg Gln Val Ile Lys Gln Leu Asp Ala Ser Glu		
340	345	350
Ile Asn Ala Gln Pro Ala Pro Val Val Glu Asn Glu Val Ala Lys Asn		
355	360	365
Arg Asp Asn Ser Pro Val Ile Thr Gln Ala Phe Phe Trp Pro Arg Val		
370	375	380
Gly Glu Phe Leu Lys Lys Asn Asp Ile Val Ile Thr Glu Thr Gly Thr		
385	390	395
Ala Asn Phe Gly Ile Trp Asp Thr Lys Phe Pro Ser Gly Val Thr Ala		400
405	410	415
Leu Ser Gln Val Leu Trp Gly Ser Ile Gly Trp Ser Val Gly Ala Cys		
420	425	430
Gln Gly Ala Val Leu Ala Ala Asp Asp Asn Ser Asp Arg Arg Thr		
435	440	445
Ile Leu Phe Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Leu		
450	455	460
Ser Thr Met Ile Arg Leu Lys Leu Lys Pro Ile Ile Phe Val Ile Cys		
465	470	475
Asn Asp Gly Phe Thr Ile Glu Arg Phe Ile His Gly Met Glu Ala Glu		480
485	490	495
Tyr Asn Asp Ile Ala Asn Trp Asp Phe Lys Ala Leu Val Asp Val Phe		
500	505	510
Gly Gly Ser Lys Thr Ala Lys Lys Phe Ala Val Lys Thr Lys Asp Glu		
515	520	525
Leu Asp Ser Leu Leu Thr Asp Pro Thr Phe Asn Ala Ala Glu Cys Leu		
530	535	540
Gln Phe Val Glu Leu Tyr Met Pro Lys Glu Asp Ala Pro Arg Ala Leu		
545	550	555
Ile Met Thr Ala Glu Ala Ser Ala Arg Asn Asn Ala Lys Thr Glu		560
565	570	575